

SEQUENCE LISTING

<110> Anderson, Annaliesa S.
Montgomery, Donna L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21490YP

<140> 10/589,381

<141> 2006-08-15

<150> PCT/US2005/004431

<151> 2005-02-14

<150> 60/545,447

<151> 2004-02-18

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 260

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> truncated derivative of sai-1

<400> 1

Met 1	Gly	Thr	Gln	Val 5	Ser	Gln	Ala	Thr	Ser 10	Gln	Pro	Ile	Asn	Phe 15	Gln
Val	Gln	Lys	Asp 20	Gly	Ser	Ser	Glu	Lys 25	Ser	His	Met	Asp	Asp 30	Tyr	Met
Gln	His	Pro 35	Gly	Lys	Val	Ile	Lys 40	Gln	Asn	Asn	Lys	Tyr 45	Tyr	Phe	Gln
Thr	Val 50	Leu	Asn	Asn	Ala	Ser 55	Phe	Trp	Lys	Glu	Tyr 60	Lys	Phe	Tyr	Asn
Ala 65	Asn	Asn	Gln	Glu	Leu 70	Ala	Thr	Thr	Val	Val 75	Asn	Asp	Asn	Lys	Lys 80
Ala	Asp	Thr	Arg	Thr 85	Ile	Asn	Val	Ala	Val 90	Glu	Pro	Gly	Tyr	Lys 95	Ser
Leu	Thr	Thr	Lys 100	Val	His	Ile	Val	Val 105	Pro	Gln	Ile	Asn	Tyr 110	Asn	His
Arg	Tyr	Thr 115	Thr	His	Leu	Glu	Phe 120	Glu	Lys	Ala	Ile	Pro 125	Thr	Leu	Ala
Asp	Ala 130	Ala	Lys	Pro	Asn	Asn 135	Val	Lys	Pro	Val	Gln 140	Pro	Lys	Pro	Ala
Gln 145	Pro	Lys	Thr	Pro	Thr 150	Glu	Gln	Thr	Lys	Pro 155	Val	Gln	Pro	Lys	Val 160
Glu	Lys	Val	Lys	Pro 165	Thr	Val	Thr	Thr	Thr 170	Ser	Lys	Val	Glu	Asp 175	Asn
His	Ser	Thr 180	Lys	Val	Val	Ser	Thr 185	Asp	Thr	Thr	Lys	Asp 190	Gln	Thr	Lys
Thr	Gln 195	Thr	Ala	His	Thr	Val	Lys 200	Thr	Ala	Gln	Thr	Ala 205	Gln	Glu	Gln
Asn	Lys 210	Val	Gln	Thr	Pro	Val 215	Lys	Asp	Val	Ala	Thr 220	Ala	Lys	Ser	Glu

Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys
 225 230 235 240
 Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser Lys Ala Lys Glu
 245 250 255
 Leu Pro Lys Thr
 260

<210> 2
 <211> 264
 <212> PRT
 <213> S. aureus

<220>

<400> 2
 Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln
 1 5 10 15
 Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met
 20 25 30
 Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln
 35 40 45
 Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn
 50 55 60
 Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asp Lys Lys
 65 70 75 80
 Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser
 85 90 95
 Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His
 100 105 110
 Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala
 115 120 125
 Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala
 130 135 140
 Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val
 145 150 155 160
 Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys Asn Glu Asn Arg
 165 170 175
 Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys Asp Gln Ser Gln
 180 185 190
 Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr Ala Gln Asp Gln
 195 200 205
 Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu
 210 215 220
 Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys
 225 230 235 240
 Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro Ser Lys Asp Ser
 245 250 255
 Lys Ala Lys Glu Leu Pro Lys Thr
 260

<210> 3
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino His-tagged construct of SEQ ID NO: 1

<400> 3
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

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Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro
      20      25      30
Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met
      35      40      45
Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys
      50      55      60
Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr
      65      70      75      80
Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn
      85      90      95
Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro
      100      105      110
Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile
      115      120      125
Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile
      130      135      140
Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln
      145      150      155      160
Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val
      165      170      175
Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser Lys
      180      185      190
Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys
      195      200      205
Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr
      210      215      220
Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr
      225      230      235      240
Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln
      245      250      255
Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser
      260      265      270
Lys Ala Lys Glu Leu Pro Lys Thr
      275      280

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<210> 4

<211> 284

<212> PRT

<213> Artificial Sequence

<220>

<223> amino His-tagged construct of SEQ ID NO: 2

<400> 4

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
  1      5      10      15
Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro
      20      25      30
Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met
      35      40      45
Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys
      50      55      60
Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr
      65      70      75      80
Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn
      85      90      95
Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro
      100      105      110
Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile
      115      120      125

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Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile
 130      135      140
Pro Thr Leu Ala Asp Ala Lys Pro Asn Asn Val Lys Pro Val Gln
145      150      155      160
Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val
      165      170      175
Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys
      180      185      190
Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys
      195      200      205
Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr
      210      215      220
Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr
225      230      235      240
Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln
      245      250      255
Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro
      260      265      270
Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr
      275      280

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<210> 5

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 1

<400> 5

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Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln
 1      5      10      15
Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met
      20      25      30
Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln
      35      40      45
Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn
      50      55      60
Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys Lys
      65      70      75      80
Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser
      85      90      95
Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His
      100      105      110
Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala
      115      120      125
Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala
      130      135      140
Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val
      145      150      155      160
Glu Lys Val Lys Pro Thr Val Thr Thr Thr Ser Lys Val Glu Asp Asn
      165      170      175
His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys Asp Gln Thr Lys
      180      185      190
Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr Ala Gln Glu Gln
      195      200      205
Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu
      210      215      220
Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys
      225      230      235      240

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Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Ala	Lys	Glu
				245					250					255	
Leu	Pro	Lys	Thr	Leu	Glu	His	His	His	His	His	His				
			260					265							

<210> 6

<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> amino His-tagged construct of SEQ ID NO: 7

<400> 6

Met	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser
1				5					10					15	
Gly	Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp
		20						25					30		
Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Asp	Lys	Ala	Met	Gly	Thr	Lys
		35				40						45			
His	Tyr	Leu	Asn	Ser	Lys	Tyr	Gln	Ser	Glu	Gln	Arg	Ser	Ser	Ala	Met
	50				55						60				
Lys	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly	Ser	Leu	Val
65				70					75					80	
Tyr	Ile	Gly	Ala	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr
			85						90				95		
Asn	Ala	Thr	Asn	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln
		100						105					110		
Pro	Ile	Asn	Phe	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His
	115						120					125			
Met	Asp	Asp	Tyr	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn
	130				135						140				
Lys	Tyr	Tyr	Phe	Gln	Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu
145				150					155					160	
Tyr	Lys	Phe	Tyr	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val
			165						170					175	
Asn	Asp	Asn	Lys	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu
		180						185					190		
Pro	Gly	Tyr	Lys	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln
	195					200						205			
Ile	Asn	Tyr	Asn	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala
	210				215						220				
Ile	Pro	Thr	Leu	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val
225			230						235					240	
Gln	Pro	Lys	Pro	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro
			245						250					255	
Val	Gln	Pro	Lys	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser
		260						265					270		
Lys	Val	Glu	Asp	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr
	275					280						285			
Lys	Asp	Gln	Thr	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln
	290				295						300				
Thr	Ala	Gln	Glu	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala
305				310					315					320	
Thr	Ala	Lys	Ser	Glu	Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser
			325						330					335	
Gln	Gln	Thr	Asn	Lys	Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala
		340					345					350			
Ser	Lys	Ala	Lys	Glu	Leu	Pro	Lys	Thr	Gly	Leu	Thr	Ser	Val	Asp	Asn
	355					360						365			

Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu Gly Ser Leu
 370 375 380
 Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 385 390 395

<210> 7
 <211> 350
 <212> PRT
 <213> S. aureus

<400> 7
 Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
 1 5 10 15
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
 20 25 30
 Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
 35 40 45
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
 50 55 60
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65 70 75 80
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85 90 95
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
 100 105 110
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
 115 120 125
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
 130 135 140
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
 145 150 155 160
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
 165 170 175
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
 180 185 190
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
 210 215 220
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
 225 230 235 240
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
 245 250 255
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
 260 265 270
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
 275 280 285
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
 290 295 300
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
 305 310 315 320
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
 325 330 335
 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 340 345 350

<210> 8
 <211> 354
 <212> PRT
 <213> S. aureus

<400> 8

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Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
 1      5      10      15
Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
 20      25      30
Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
 35      40      45
Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
 50      55      60
Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65      70      75
Lys Ser His Met Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85      90      95
Gln Asn Asn Lys Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe
100      105      110
Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
115      120      125
Thr Val Val Asn Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
130      135      140
Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
145      150      155
Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
165      170      175
Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
180      185      190
Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
195      200      205
Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr
210      215      220
Ala Pro Ser Lys Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser
225      230      235
Glu Ala Thr Lys Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys
245      250      255
Thr Thr Gln Thr Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys
260      265      270
Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
275      280      285
Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His
290      295      300
Lys Gln Gly Pro Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr
305      310      315
Gly Leu Thr Ser Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr
325      330      335
Leu Ala Leu Leu Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu
340      345      350
Ser Lys

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<210> 9

<211> 358

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 7

<400> 9

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Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
 1      5      10      15
Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
 20      25      30

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Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
   35           40           45
Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
   50           55           60
Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
   65           70           75           80
Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
           85           90           95
Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
           100          105          110
Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
           115          120          125
Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
           130          135          140
Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
           145          150          155          160
Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
           165          170          175
Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
           180          185          190
Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
           195          200          205
Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
           210          215          220
Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
           225          230          235          240
Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
           245          250          255
Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
           260          265          270
Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
           275          280          285
Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
           290          295          300
Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
           305          310          315          320
Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
           325          330          335
Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys Leu Glu
           340          345          350
His His His His His
           355

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<210> 10

<211> 843

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 3

<400> 10

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atgggcagca gccatcatca tcatcatcac agcagcggcc tgggtgccgcg cggcagccat 60
atgggcacac aagtttctca agcaacatca caaccaatta atttccaagt gcaaaaagat 120
ggctcttcag agaagtcaca catggatgac tatatgcaac accctggtaa agtaattaaa 180
caaaataata aatattattt ccaaaccgtg ttaaacaatg catcattctg gaaagaatac 240
aaattttaca atgcaaacaa tcaagaatta gcaacaactg ttgttaacga taataaaaaa 300
gcggatacta gaacaatcaa tgttgcagtt gaacctggat ataagagctt aactactaaa 360
gtacatatgg tcgtgccaca aattaattac aatcatagat atactacgca tttggaattt 420
gaaaaagcaa ttcctacatt agctgacgca gcaaaaccaa acaatgttaa accggttcaa 480
ccaaaaccag ctcaacctaa aacacctact gagcaaacta aaccagttca acctaaagtt 540

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```

gaaaaagtta aacctactgt aactacaaca agcaaagttg aagacaatca ctctactaaa 600
gttgtaagta ctgacacaac aaaagatcaa actaaaacac aaactgctca tacagttaaa 660
acagcacaaa ctgctcaaga acaaaaataaa gttcaaacac ctgttaaaga tgttgcaaca 720
gcgaaatctg aaagcaacaa tcaagctgta agtgataata aatcacaaca aactaacaaa 780
gttacaaaac ataacgaaac gcctaaacaa gcatctaaag ctaaagaatt accaaaaaact 840
tga 843

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<210> 11

<211> 855

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence encoding SEQ ID NO: 4

<400> 11

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atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat 60
atgggcacac aagtttctca agcaacatca caaccaatta atttccaagt gcaaaaagat 120
ggctcttcag agaagtcaca catggatgac tatatgcaac accctggtaa agtgattaaa 180
caaaataata aatattattht ccaagctgta ttgaacaacg catcattctg gaaagaatac 240
aaattttaca atgcaaacaa tcaagaatta gcaacaactg ttgttaacga tgataaaaaa 300
gctgacacta gaacaatcaa tgttgctggt gaacctgggt ataagagttt aactacaaaa 360
gtacatattht tcgtgccaca aattaattat aatcatagat atactacgca tttagaattht 420
gaaaaagcaa ttcctacatt agctgacgca gcaaaaccaa acaatgttaa accggttcaa 480
ccaaaacctg ctcaacctaa aacacctact gagcaaacga aaccagttca acctaaagtt 540
gaaaaagtta aacctgctgt aactgcacca agcaaaaatg aaaacagaca aactacaaaa 600
gttgtaagta gtgaagctac aaaagatcaa agtcaaacac aaagtgctcg tacagtgaag 660
acaacacaaa cagctcaaga tcaaaaataaa gttcaaacac ctgttaaaga tgttgcaaca 720
gcgaaatctg aaagcaacaa tcaagctgta agtgacaata aatcacaaca aactaacaaa 780
gttacaaaac aaaacgaagt tcataaacaa ggaccttcaa aagattctaa agctaaagaa 840
ttacacaaaaa ctthg 855

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<210> 12

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

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gagatatacc atgggcacaa aacattattht aaacagt 37

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<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

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ccggcggccc tcgagtttag attctthtct tttgaa 36

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<210> 14

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14
 gagatataacc atgggcacaa aacattatTT aaacagt 37
 <210> 15
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 15
 ccggcggccc tcgagttatt tagattcttt tcttttgaa 39
 <210> 16
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 16
 gagatatacc atgggcacac aagtttctca agcaacatca c 41
 <210> 17
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 17
 ggtggtgctc gagagttttt ggtaattctt tagctt 36
 <210> 18
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 18
 gagatatcat atgggcacac aagtttctca agcaacatca c 41
 <210> 19
 <211> 39
 <212> DNA
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21490YP

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<223> LPXTG Motif

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<221> SITE

<222> (3)...(3)

<223> Xaa = any amino acid

<400> 20

Leu Pro Xaa Thr Gly

1

5